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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/090,002	03/05/2002	Chunhua Yan	CL001316	4439

25748 7590 08/22/2003

CELERA GENOMICS CORP.
ATTN: WAYNE MONTGOMERY, VICE PRES, INTEL PROPERTY
45 WEST GUDE DRIVE
C2-4#20
ROCKVILLE, MD 20850

EXAMINER	
STEADMAN, DAVID J	

ART UNIT	PAPER NUMBER
1652	13

DATE MAILED: 08/22/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

FILE COPY

Office Action Summary	Application No.	Applicant(s)	
	10/090,002	YAN ET AL.	
	Examiner	Art Unit	
	David J Steadman	1652	

-- The MAILING DATE f this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *20 June 2003* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *4,8,9 and 24-37* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *4,8,9 and 24-37* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *05 March 2002* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Pri rity under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *sequence alignment* .

DETAILED ACTION

Status of the Application

[1] Claims 4, 8, 9, and 24-37 are pending in the application.

[2] Applicant's cancellation of claims 1-3, 5-7, and 10-23 and addition of claims 24-37 in Paper No. 12, filed June 20, 2003, is acknowledged.

[3] Applicant's election without traverse of Group III, original claims 4-6, 8-11, 22, and 23, drawn to an isolated nucleic acid encoding SEQ ID NO:2 in Paper No. 12 is acknowledged.

Oath/Declaration

[4] It is noted that the declaration filed as Paper No. 5 has not been signed by inventor Gong as required under 37 CFR § 1.63(a)(1). Applicant's petition under 37 CFR § 1.47(a), filed as Paper No. 9, has been granted and the instant application has been afforded 37 CFR § 1.47(a) status (see Paper No. 10 for details regarding granting of the petition).

Sequence Compliance

[5] This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825; applicants' attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). To be in compliance, applicant is required to identify all amino acid sequences of at least 4 L-amino acids and at least 10 nucleotides by a sequence identifier, i.e., "SEQ ID NO:". The specification discloses sequences that have not been identified by a sequence identifier (see Figure 2A). If these sequences have not been disclosed in the computer readable form of the sequence listing and the paper copy thereof, applicant must provide a computer readable form copy of the "Sequence Listing" including these sequences, a paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification, and a statement that the content of the paper and CRF copies are the same and,

where applicable, include no new matter as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.821(b) or 1.825(d).

Specification/Informalities

[6] The attempt to incorporate subject matter into this application by reference to a hyperlink embedded in the specification (see particularly page 11, lines 22 and 26) is improper. Incorporation of subject matter into the patent application by reference to a hyperlink and/or other forms of browser-executable code is considered to be an improper incorporation by reference. See MPEP 608.01 regarding hyperlinks in the specification and 608.01(p), paragraph I regarding incorporation by reference.

Claim Rejections - 35 USC § 112, Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

[7] Claims 25 and 27 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 25 and 27 are indefinite in the recitation of "having a nucleotide sequence consisting of". The scope of claimed polynucleotides is unclear because the claims recite the term "having", which, according to MPEP § 2111.03, can be interpreted as open or closed claim language and is typically interpreted as open claim language in claims drawn to nucleic acid sequences and further recite "consisting of", which according to MPEP § 2111.03, is closed claim language. It is noted that if the term "having" in claim 25 were interpreted as using open claim language, claims 25 and 26 would be identical in scope and claim 26 would be a substantial duplicate of claim 25. In view of the duplicity of claims 25 and 26 (if the term "having" in claim 25 were interpreted as open language), the examiner has interpreted the term "having" in claims 25 and 27 as closed claim language and claims 25 and 27 have

been essentially interpreted as "[a]n isolated polynucleotide consisting of SEQ ID NO:1" and "[a]n isolated polynucleotide consisting of SEQ ID NO:3", respectively. Because the term "having" is typically interpreted as open claim language in claims drawn to nucleic acid sequences, it is suggested that applicant clarify the scope of claimed polynucleotides by, for example, amending the term "having a nucleotide sequence consisting of" to "consisting of" in claims 25 and 27.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

[8] Claims 4, 8, and 28 are rejected under 35 U.S.C. 102(b) as being anticipated by Database GenBank Accession Number AC022382 (version AC022382.3, gi:12007691). Claim 4 (in relevant part) is drawn to an isolated nucleic acid molecule consisting of a nucleotide sequence that encodes a polypeptide having an amino acid sequence comprising SEQ ID NO:2. Claim 8 is drawn to a vector comprising the nucleic acid molecule of claim 4. Claim 28 limits the vector of claim 4 to a plasmid, a virus, or a bacteriophage. Database GenBank Accession Number AC022382 teaches a genomic nucleic acid sequence that is identical to SEQ ID NO:3 with the exception that nucleotide 70,879 of Database GenBank Accession Number AC022382 is not present, i.e., is deleted, in SEQ ID NO:3 (see attached sequence alignment). According to the specification (see Figures 3F and 3G), the deletion is within an intron of SEQ ID NO:3. Thus, although the sequences of Database GenBank Accession Number AC022382 and SEQ ID NO:3 are not 100% identical, the nucleic acid sequence of Database GenBank Accession Number AC022382 nonetheless encodes SEQ ID NO:2 as this deletion (as described above) does not occur in an exon (polypeptide coding sequence) of SEQ ID NO:3. Database GenBank Accession Number

AC022382 further teaches their nucleic acid is present in a pUC18 vector for sequencing (see "Comment" section). This anticipates claims 4, 8, and 28 as written.

Claim Rejections - 35 USC § 102/103

[9] Claim 9 is rejected under 35 U.S.C. 102(b) as anticipated by or, in the alternative, under 35 U.S.C. 103(a) as obvious over Database GenBank Accession Number AC022382. Database GenBank Accession Number AC022382 discloses the teachings as set forth in item 8 above. Database GenBank Accession Number AC022382 further teaches the sequence of their nucleic acid was determined from clone RP11-266J6. One of ordinary skill in the art would recognize the meaning of the term "clone" in the context of Database GenBank Accession Number AC022382 refers to a host cell comprising a vector and that, in the course of cloning the nucleic acid of Database GenBank Accession Number AC022382 into the disclosed pUC18 vector, the vector would necessarily be used to transform a host cell for replication of the vector for sequencing. Therefore, while Database GenBank Accession Number AC022382 does not specifically teach that the pUC18 vector comprising their nucleic acid sequence is present in a host cell, transformation of a host cell with a vector is an inherent feature of generating a clone and thus, the pUC18 vector comprising the nucleic acid sequence of Database GenBank Accession Number AC022382 would necessarily be present in a host cell. Alternatively, it would be obvious to one of ordinary skill in the art to transform a host cell with the pUC18 vector comprising the nucleic acid sequence of Database GenBank Accession Number AC022382 in order to replicate the plasmid for nucleotide sequencing. One of ordinary skill in the art would have been motivated to transform a host cell with the pUC18 vector comprising the nucleic acid sequence of Database GenBank Accession Number AC022382 in order to generate the required amount of plasmid for sequencing.

[10] It is noted that, while Database GenBank Accession Number AC022382 teaches their nucleic acid is inserted into a pUC18 cloning vector, claim 24, drawn to a process for producing a polypeptide comprising culturing the host cell of claim 9 and recovering the polypeptide and claims 29 and 30, drawn

to the vector of claim 8, wherein the nucleic acid molecule is inserted into the vector in proper orientation and correct reading frame such that a polypeptide comprising SEQ ID NO:2 may be expressed in a host cell (claim 29) and optionally wherein said nucleic acid molecule is operatively linked to a promoter sequence (claim 30), have not been rejected as being anticipated or made obvious by Database GenBank Accession Number AC022382. In the instant case, the pUC18 vector as disclosed in Database GenBank Accession Number AC022382 is a vector used for cloning, sequencing and site-directed mutagenesis and does not possess the necessary promoter for polypeptide expression (see Norrander et al. *Gene* 26:101-106 describing the construction of pUC18). Database GenBank Accession Number AC022382 teaches their nucleic acid is a genomic human nucleic acid sequence. It is well known to one of ordinary skill in the art that pUC18 is replicable in bacterial cells and not eucaryotic cells, and thus a skilled artisan would not be motivated to transfect a eucaryotic host cell with the vector of Database GenBank Accession Number AC022382. Also, even if the nucleic acid were transcribed into mRNA in a bacterial cell, it would not be processed into a SEQ ID NO:2-encoding nucleic acid as bacterial mRNA does not undergo post-transcriptional processing. Furthermore, Database GenBank Accession Number AC022382 provides no indication that their nucleic acid is a protein-encoding sequence, thus, there would be no motivation to remove the nucleic acid of Database GenBank Accession Number AC022382 and insert this nucleic acid into a eucaryotic expression vector, transfect a eucaryotic host cell with said eucaryotic expression vector, and produce a polypeptide using said eucaryotic host cell. Thus, claims 24, 29, and 30 have not been rejected as being anticipated or rendered obvious by Database GenBank Accession Number AC022382.

Double Patenting

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington,* 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

[11] Claims 4, 8, 9, 24-26, and 28-37 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 4, 5, and 8-11 of copending Application No. 10/300,828 (hereafter referred to as "Application '828"). An obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but an examined application claim is not patentably distinct from the reference claim(s) because the examined claim is either anticipated by, or would have been obvious over, the reference claim(s). See *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); and *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985). Although the conflicting claims are not identical, they are not patentably distinct from each other. Claims 4, 8, 9, 24-26, and 28-37 of the instant application and claims 4, 5, and 8-11 of Application '828 are both directed to an isolated nucleic acid encoding SEQ ID NO:2 and a complement thereof, a vector comprising said nucleic acid, a host cell containing said vector, and a method of making a polypeptide. The claims differ in that the nucleic acids of claims 4 and 5 of Application '828 encompass nucleic acids encoding variants and fragments of SEQ ID NO:2, claims 4(b), 25, 26, and 31(b) of the instant application are limited to SEQ ID NO:1, claim 31(a) of the instant application is limited to a transcript/cDNA encoding SEQ ID NO:2, and the process and vectors of claims 24, 28-30, and 32-37 of the instant application are further limited to embodiments not recited in claims 8, 10, and 11 of Application '828. It is noted that SEQ ID NO:1 of the instant application is a fragment of SEQ ID NO:1 of Application '828 that is 100% identical to nucleotides 135 to 1115 of SEQ ID NO:1 of Application '828. The specification of Application '828 discloses an embodiment within the scope of the genus of claims 4, 5, and 8-11 of Application '828 which supports said genus and that would anticipate claims 4, 8, and 9 herein, i.e., an isolated nucleic acid encoding SEQ ID NO:2 and a complement thereof (e.g., claims 4(a) and 4(e) and 5(a) and 5(e) of Application '828), a vector

comprising an isolated nucleic acid encoding SEQ ID NO:2 (e.g., claim 8 of Application '828), and a host cell containing said vector (e.g., claim 9 of Application '828). Claims 4, 8, and 9 cannot be considered to be patentably distinct over claims 4, 5, 8, and 9 of Application '828 when there is a specifically recited embodiment in Application '828 that would anticipate claims 4, 8, and 9 of the instant application. Alternatively, claims 4, 8, 9, 24-26, and 28-37 cannot be considered patentably distinct over claims 4, 5, and 8-11 of Application '828 when there are specifically disclosed embodiments in Application '828 that support claims 4, 5, and 8-11 of Application '828 and fall within the scope of claims 4, 8, 9, 24-26, and 28-37 herein because the following specifically disclosed embodiments of Application '828 would have been obvious to one of ordinary skill in the art from the claimed genus of Application '828 based on the cited teachings of the specification of Application '828, which support the genus: the nucleic acid encoding SEQ ID NO:2 of claims 4 or 5 of Application '828 to be a nucleic acid comprising SEQ ID NO:1 or comprising or consisting of the full open reading frame (nucleotides 135 to 1115) of SEQ ID NO:1 (see Figure 1A, page 6, lines 24-29, and page 30, lines 10-15 of Application '828); the nucleic acid encoding SEQ ID NO:2 of claims 4 or 5 of Application '828 to be a transcript/cDNA sequence (see page 31, line 5 of Application '828); the vector and host cell of claims 8 and 9 of Application '828 to be a vector comprising a nucleic acid comprising or consisting of SEQ ID NO:1 or the open reading frame of SEQ ID NO:1 or a transcript/cDNA encoding SEQ ID NO:2 and a host cell containing said vector (see claims 8 and 9 of Application '828); to practice the methods of claims 10 and 11 of Application '828 using the host cell of claim 9 containing a vector comprising a nucleic acid or transcript/cDNA encoding SEQ ID NO:2, a vector comprising SEQ ID NO:1 or consisting of the open reading frame of SEQ ID NO:1 and recovering said polypeptide (see page 50, lines 9-11 of Application '828); the vector of claim 8 of Application '828 to be a plasmid, a virus, or a bacteriophage (see page 46, lines 4-9 of Application '828), to have the nucleic acid molecule inserted into the vector such that the polypeptide of SEQ ID NO:2 may be expressed (see page 45, lines 8-22 of Application '828), and optionally to have the nucleic acid molecule operatively linked to a promoter sequence (see page 45, lines 18-22 of Application '828). This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Conclusion

[12] Status of the claims:

- Claims 4, 8, 9, and 24-37 are pending.
- Claims 4, 8, 9, and 24-37 are rejected.
- No claim is in condition for allowance.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David Steadman, whose telephone number is (703) 308-3934. The Examiner can normally be reached Monday-Friday from 7:00 am to 5:00 pm. If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Ponnathapura Achutamurthy, can be reached at (703) 308-3804. The FAX number for submission of official papers to Group 1600 is (703) 308-4242. Draft or informal FAX communications should be directed to (703) 746-5078. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Art Unit receptionist whose telephone number is (703) 308-0196.

David J. Steadman
Patent Examiner
Art Unit 1652

08/20/03

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 11, 2003, 14:34:44 ; Search time 2056 Seconds
(without alignments)
2.772 Million cell updates/sec

Title: us-10-090-002-3
Perfect score: 15400
Sequence: 1 aaaccgacctttggcctctt.....atgtggccgggagcagtggc 15400

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 185061 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : 12008691.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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ALIGNMENTS

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DEFINITION Homo sapiens chromosome 3 clone RP11-266J6 map 3p, complete sequence.
ACCESSION AC022382
VERSION AC022382.3 GI:12007691
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 185061)
AUTHORS Bao,W., Bao,J., Bao,Q., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
TITLE Chromosome 3p genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 185061)
AUTHORS Wu,D., Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wang,X., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J. and Yang,H.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China
REFERENCE 3 (bases 1 to 185061)
AUTHORS Bao,W., Bao,J., Bao,Q., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
TITLE Direct Submission
JOURNAL Submitted (02-JAN-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China
COMMENT [WARNING] On Nov 13, 2002 this sequence was replaced by a newer version gi:24942870.
On Jan 2, 2001 this sequence version replaced gi:8101170.
--------------Genome Center
Center:Beijing Center
Center code:Beijing
Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
-------------- Project Information
Center project name:1% project
Center clone name: RP11-266J6
-------------- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 86 bases at least Q40
Consensus quality: 264 bases at least Q30
Consensus quality: 378 bases at least Q20
Insert size: 812; sum-of-contigs
Quality coverage: 0.60x in Q20 bases;sum-of-contigs

FEATURES Location/Qualifiers
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/map="3p"
/clone="RP11-266J6"
BASE COUNT 47254 a 46299 c 45835 g 45673 t

Query Match 99.9%; Score 15389.5; DB 1; Length 185061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 15400; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64776 AAACCGACCTTTGGCCTCTTGCCTGCCGTCCTAGTTGCAGGCTCTCTCCCCTAACCTGGA 64835

Qy         61 CCCCAGCCATCAAACTCTGGAGCCCCGCCAGTCACGTGACACCTCGGTCCTTTTTGGCCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 GTTTCCTTCAGGATCCCGATTTAACTTCCTCCTCCCCAATTCCCTCTGCCCCCAATACCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64896 GTTTCCTTCAGGATCCCGATTTAACTTCCTCCTCCCCAATTCCCTCTGCCCCCAATACCT 64955
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Qy       2401 TGGGGAGCTCCAGCTGTGGCTGTTGTTGCTGTGGTAACAGTGCAGAAAGAGCTATTTAAA 2460
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Qy       2461 AATGTGGCTGAGATGTTGCTGGAAGCCCAGGCTGCTGGAAACCTGATTTCGGAGAGGCCG 2520
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Qy       2521 GGGAGTCGGGGGAAGGAGGAGGGAAAGGAGACACCCCAGCAATCCCCAGGGTGGGGCGGG 2580
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Db      67296 GGGAGTCGGGGGAAGGAGGAGGGAAAGGAGACACCCCAGCAATCCCCAGGGTGGGGCGGG 67355

Qy       2581 GACATCACTGGTTCTGGGGACAGGGGGATCCTCCAGGCTTCTACCAGCTGCTCTGGGGGT 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67356 GACATCACTGGTTCTGGGGACAGGGGGATCCTCCAGGCTTCTACCAGCTGCTCTGGGGGT 67415

Qy       2641 TTATCTGTTGTACTGCCAGAAGTCAGGGTTTCCCTAGGTGCTTGGATTTGGATAGGGGGA 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67416 TTATCTGTTGTACTGCCAGAAGTCAGGGTTTCCCTAGGTGCTTGGATTTGGATAGGGGGA 67475

Qy       2701 AAACTGGGAAGAGAACTAGAATAAATGAATGAATGAATGCATGACTTTGTTAAATAAAGA 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67476 AAACTGGGAAGAGAACTAGAATAAATGAATGAATGAATGCATGACTTTGTTAAATAAAGA 67535

Qy       2761 ATTTTGCTGCCACTGTGAAAGGTTTTTCTCTAGGCATGAGAATTTGCTGAATGTTGAATA 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67536 ATTTTGCTGCCACTGTGAAAGGTTTTTCTCTAGGCATGAGAATTTGCTGAATGTTGAATA 67595

Qy       2821 AACAAATGAATGTTTGTTGAATGATTTTGTCAAATGGATGAATCAAGGATGAATAAATGC 2880
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Db      67596 AACAAATGAATGTTTGTTGAATGATTTTGTCAAATGGATGAATCAAGGATGAATAAATGC 67655

Qy       2881 AGGTTGAATGACTGAATGGGGCCTGCAGTAAATTCCCAGACAGAGGGCTGGGCTCTGCTG 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67656 AGGTTGAATGACTGAATGGGGCCTGCAGTAAATTCCCAGACAGAGGGCTGGGCTCTGCTG 67715

Qy       2941 AGTCTCCTCCTTCCATTCTCCTTACAGGAGCCCTGGCTGTGGTCGGGGGGCAGTGGGCCA 3000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67716 AGTCTCCTCCTTCCATTCTCCTTACAGGAGCCCTGGCTGTGGTCGGGGGGCAGTGGGCCA 67775

Qy       3001 TGCTGGGGGCAGTGGAAGGCCCCAGGTGGAAGCAGGCGGAGGACATTAGAGACATCTACG 3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67776 TGCTGGGGGCAGTGGAAGGCCCCAGGTGGAAGCAGGCGGAGGACATTAGAGACATCTACG 67835

Qy       3061 ACTTCCGAGATGTTCTGGGCACGTGAGTCCAGGGCAGGATTGGGTGCTGGATGGCTGAGG 3120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67836 ACTTCCGAGATGTTCTGGGCACGTGAGTCCAGGGCAGGATTGGGTGCTGGATGGCTGAGG 67895

Qy       3121 GAGGCTGAGTCCAGGGTGGGGCTTCCTCTGGTCAATTAATGCTTCCTGTTTCCCACAGCC 3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67896 GAGGCTGAGTCCAGGGTGGGGCTTCCTCTGGTCAATTAATGCTTCCTGTTTCCCACAGCC 67955

Qy       3181 CAGGCCCTGTGGCAGCACTATCTAGGGCCTAAACTGTCCCCAGCTTTTCACTTCTGGATG 3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67956 CAGGCCCTGTGGCAGCACTATCTAGGGCCTAAACTGTCCCCAGCTTTTCACTTCTGGATG 68015

Qy       3241 ACAGTGGGTGGGACACGGGCTGCTCTCCCAATAGCCCTGGGTTCTTGAAGAGAAAGAAGT 3300
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Db      68016 ACAGTGGGTGGGACACGGGCTGCTCTCCCAATAGCCCTGGGTTCTTGAAGAGAAAGAAGT 68075

Qy       3301 CGAGAGAATGAAGGTGCCAGTCAGTCCATTTAACTTGCTGCCAAGAGCTAAGTGTTCTAG 3360
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Db      68076 CGAGAGAATGAAGGTGCCAGTCAGTCCATTTAACTTGCTGCCAAGAGCTAAGTGTTCTAG 68135

Qy       3361 CCTAGGTTTGGGAACTGAGGCTGGAGATGGCTCTGTTCTTGGTGCTGGGAATGCAGAAAT 3420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68136 CCTAGGTTTGGGAACTGAGGCTGGAGATGGCTCTGTTCTTGGTGCTGGGAATGCAGAAAT 68195

Qy       3421 AACTCAAACCTGGTCTCTGCCCTTCAAGTTGATCCCAGACATGTGCAAGAGACAGACCTA 3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68196 AACTCAAACCTGGTCTCTGCCCTTCAAGTTGATCCCAGACATGTGCAAGAGACAGACCTA 68255

Qy       3481 CAGAAAATGACAACAGGGTGTGTGCTGTGCTCCAATTAAGGTTGGGATTGAGGGCTTTGT 3540
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Db      68256 CAGAAAATGACAACAGGGTGTGTGCTGTGCTCCAATTAAGGTTGGGATTGAGGGCTTTGT 68315

Qy       3541 GGAGCCCAGAGAGAGCTGTGCCTTCTGCCTGGGGGAAAACTTCCTGGAGAATGGGGCATT 3600
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Db      68316 GGAGCCCAGAGAGAGCTGTGCCTTCTGCCTGGGGGAAAACTTCCTGGAGAATGGGGCATT 68375

Qy       3601 AGAGCTGGGGACTGAAGGATGGGTAGGTGTGCACTTGTCAGAGAGGAAGAAGGACATTCC 3660
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Db      68376 AGAGCTGGGGACTGAAGGATGGGTAGGTGTGCACTTGTCAGAGAGGAAGAAGGACATTCC 68435

Qy       3661 AGGCAGAAGGAATAGCATAAACAAAGGCTTAGAGGCATGGTTCTATGTGGAGAGAGGTAG 3720
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Db      68436 AGGCAGAAGGAATAGCATAAACAAAGGCTTAGAGGCATGGTTCTATGTGGAGAGAGGTAG 68495

Qy       3721 AGTGTGATGGAGCTTAAAATCACAGGCTGGGGGGAGAGTGGAAAAAGGGGCTGGAGATGA 3780
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Db      68496 AGTGTGATGGAGCTTAAAATCACAGGCTGGGGGGAGAGTGGAAAAAGGGGCTGGAGATGA 68555

Qy       3781 AAGTGGGACAGTTTGTGTAGGGTTTTGGAAGCCAGGCCAGGGAGGCTGGATATTGTCCCA 3840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68556 AAGTGGGACAGTTTGTGTAGGGTTTTGGAAGCCAGGCCAGGGAGGCTGGATATTGTCCCA 68615

Qy       3841 TAGGCCACCGGGAGACACTTAAGACTTTTTGGCAGGTGTGCAATTCAGGATAGTCACTCT 3900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68616 TAGGCCACCGGGAGACACTTAAGACTTTTTGGCAGGTGTGCAATTCAGGATAGTCACTCT 68675

Qy       3901 GGCCACAGCTTGGAGGGTAAATTGGAGAGGGACAAGACTGGAAACCAGTGATGAGGTTAC 3960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68676 GGCCACAGCTTGGAGGGTAAATTGGAGAGGGACAAGACTGGAAACCAGTGATGAGGTTAC 68735

Qy       3961 TACAGTAACTAATTATCCCTGAGGATTGAAATTTCACCACGAGAGATGCTTTTCTTTGAC 4020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68736 TACAGTAACTAATTATCCCTGAGGATTGAAATTTCACCACGAGAGATGCTTTTCTTTGAC 68795

Qy       4021 TTATGACTTCTTATTCTCCCAGAGAAAGCAAACAGATGTGGAAAGAATACCCTAGCAAAT 4080
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Db      68796 TTATGACTTCTTATTCTCCCAGAGAAAGCAAACAGATGTGGAAAGAATACCCTAGCAAAT 68855

Qy       4081 CCTCTTTAATCAGTTAACTTTAGTTAAATGAGTTTATTTGTTCCTTTTTAAGAACCTGTT 4140
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Db      68856 CCTCTTTAATCAGTTAACTTTAGTTAAATGAGTTTATTTGTTCCTTTTTAAGAACCTGTT 68915

Qy       4141 CTAAAACACTGCTTCTTAAAGTTCAATGAGCATACAAATCACCTGAGGATTTTGTTAAAC 4200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68916 CTAAAACACTGCTTCTTAAAGTTCAATGAGCATACAAATCACCTGAGGATTTTGTTAAAC 68975

Qy       4201 TGCAGATTGATTTAGTAAATCTGGGGCAGGGCCTAAAGTTTTGCATTTCTTTTTTTTTTC 4260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68976 TGCAGATTGATTTAGTAAATCTGGGGCAGGGCCTAAAGTTTTGCATTTCTTTTTTTTTTC 69035

Qy       4261 TTTTTTTTGACCCAGGATCCAAAGCAGTAGAGATTTTGCATTTCTAAAAAAGTTCCCGGG 4320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69036 TTTTTTTTGACCCAGGATCCAAAGCAGTAGAGATTTTGCATTTCTAAAAAAGTTCCCGGG 69095

Qy       4321 TGATGCTGATGGTTCTTTAAGGTTCTAAAGGGTGTTAAATTAGCCATGACTCGAATTAGC 4380
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Db      69096 TGATGCTGATGGTTCTTTAAGGTTCTAAAGGGTGTTAAATTAGCCATGACTCGAATTAGC 69155

Qy       4381 AGAAAAAGGGATGAACCAACTGTACACATAATCCAAAAGCCCAGGGGTAGACCTCAGGCA 4440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69156 AGAAAAAGGGATGAACCAACTGTACACATAATCCAAAAGCCCAGGGGTAGACCTCAGGCA 69215

Qy       4441 TGGCTGGATCCAGAGGGCCACATAATGTTATCAGGAAATATATTTGGCCATTTCTCAGGT 4500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69216 TGGCTGGATCCAGAGGGCCACATAATGTTATCAGGAAATATATTTGGCCATTTCTCAGGT 69275

Qy       4501 TGGACTTCCTTTGTGTTAATTTCATTCCCAAGCAGGCTCTCCCCAGGTGGTGGCAAAGAT 4560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69276 TGGACTTCCTTTGTGTTAATTTCATTCCCAAGCAGGCTCTCCCCAGGTGGTGGCAAAGAT 69335
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Db      71496 CAAACATGTAAACACAGAAAACTATATATATATATTTTTTTTGAGATGGAGTTTTGCTCT 71555

Qy       6780 TGTTGCCCAGGCTGGAGTGTAATGGCATGATCTCGACTCACTGCAACCTCCGTTTCCCAG 6839
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Db      71556 TGTTGCCCAGGCTGGAGTGTAATGGCATGATCTCGACTCACTGCAACCTCCGTTTCCCAG 71615

Qy       6840 GTTTAAGCAATTCTCCTGCCTCAGCCTCACAGATAGCTGGGATTACAGGCATGTGCCACC 6899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71616 GTTTAAGCAATTCTCCTGCCTCAGCCTCACAGATAGCTGGGATTACAGGCATGTGCCACC 71675

Qy       6900 ATGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGTTTTCGCCATGTTGGCCAGGCTG 6959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71676 ATGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGTTTTCGCCATGTTGGCCAGGCTG 71735

Qy       6960 GTCTCGAACTCCTGACCTCAAGTGATCCGCCTGCCTTGGCCTCCCAAAGTGCTGGGATTA 7019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71736 GTCTCGAACTCCTGACCTCAAGTGATCCGCCTGCCTTGGCCTCCCAAAGTGCTGGGATTA 71795

Qy       7020 CAGGTGTGAGTCTCTGTGCCTAGCCAGAAAACTCTTAAGAGGTATGTATCAGGCTGGGTG 7079
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Db      71796 CAGGTGTGAGTCTCTGTGCCTAGCCAGAAAACTCTTAAGAGGTATGTATCAGGCTGGGTG 71855

Qy       7080 CAGTGGCTCACTGGTGAAAAGATCTGCACCCAAATAGCATGTGACGGGCAGGATTTGGAC 7139
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Db      71856 CAGTGGCTCACTGGTGAAAAGATCTGCACCCAAATAGCATGTGACGGGCAGGATTTGGAC 71915

Qy       7140 CCAGGTCTGTGTATGCCAGAGCCCAGTGTTTATCCCTCTGCTCTCTCACCTTCCAAAAAA 7199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71916 CCAGGTCTGTGTATGCCAGAGCCCAGTGTTTATCCCTCTGCTCTCTCACCTTCCAAAAAA 71975

Qy       7200 TGGTAATAAACCATGGTAAGCTAGCTTTTCCCTTTGGGGACGAGATCCTTGGTTTGTCCT 7259
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Db      71976 TGGTAATAAACCATGGTAAGCTAGCTTTTCCCTTTGGGGACGAGATCCTTGGTTTGTCCT 72035

Qy       7260 ACCCAGGTATGTAGGCAGTGGTCGGGGGTTGGGGGTGGCTGAGCTGTCCTGAGCTCTAAA 7319
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Db      72036 ACCCAGGTATGTAGGCAGTGGTCGGGGGTTGGGGGTGGCTGAGCTGTCCTGAGCTCTAAA 72095

Qy       7320 CCGCTGTTTTTTTTTTTTTTTTTTTGAGACAGGGTCTTACTCTGTTGCCCAGGCTGGAGT 7379
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Db      72096 CCGCTGTTTTTTTTTTTTTTTTTTTGAGACAGGGTCTTACTCTGTTGCCCAGGCTGGAGT 72155

Qy       7380 GCAGTGGCTAGTCACAGGTGCAATCATAACAGACTGCAGCTTTGAACTGCTGGGGCCAAG 7439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72156 GCAGTGGCTAGTCACAGGTGCAATCATAACAGACTGCAGCTTTGAACTGCTGGGGCCAAG 72215

Qy       7440 TGATCCTCCTGCCTCAGCCTCCCAAGTTCCCAAGTAGCTTGGACTACAGGTGCACACCGC 7499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72216 TGATCCTCCTGCCTCAGCCTCCCAAGTTCCCAAGTAGCTTGGACTACAGGTGCACACCGC 72275

Qy       7500 CATGCCTGGCTAAACCACCTCATTTCTCCTTTCAGGATCAAGCACCCCAACATTGTAGCC 7559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72276 CATGCCTGGCTAAACCACCTCATTTCTCCTTTCAGGATCAAGCACCCCAACATTGTAGCC 72335

Qy       7560 CTGGATGACATCTATGAGAGTGGGGGCCACCTCTACCTCATCATGCAGCTGTGAGTGGCC 7619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72336 CTGGATGACATCTATGAGAGTGGGGGCCACCTCTACCTCATCATGCAGCTGTGAGTGGCC 72395

Qy       7620 CAACCTCTGCCCTGCCCCCACACCTCTCCCAGCTGTCCCAACCCTCTTTGCCAGACTGCC 7679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72396 CAACCTCTGCCCTGCCCCCACACCTCTCCCAGCTGTCCCAACCCTCTTTGCCAGACTGCC 72455

Qy       7680 CTATCCCCTGCTGCAGGGTGTCGGGTGGGGAGCTCTTTGACCGTATTGTGGAAAAAGGCT 7739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72456 CTATCCCCTGCTGCAGGGTGTCGGGTGGGGAGCTCTTTGACCGTATTGTGGAAAAAGGCT 72515

Qy       7740 TCTACACGGAGCGGGACGCCAGCCGCCTCATCTTCCAGGTGCTGGATGCTGTGAAATACC 7799
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Db      72516 TCTACACGGAGCGGGACGCCAGCCGCCTCATCTTCCAGGTGCTGGATGCTGTGAAATACC 72575

Qy       7800 TGCATGACCTGGGCATTGTACACCGGGATCTCAAGGTGGGGCTCAAGGGGGTGTGGTGAG 7859
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Db      72576 TGCATGACCTGGGCATTGTACACCGGGATCTCAAGGTGGGGCTCAAGGGGGTGTGGTGAG 72635
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Qy       7860 CTAGGGTACCCAGGGGTGGGGCCTTTGCAAACCCCAAACTGTCTGACCTTGGGCAACTTT 7919
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Db      72636 CTAGGGTACCCAGGGGTGGGGCCTTTGCAAACCCCAAACTGTCTGACCTTGGGCAACTTT 72695

Qy       7920 CACCCCCTCACTGAGCCTTGGATTTCCATCTACAAAGTGGATCTTGTAACCTTTAAACTG 7979
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Qy       7980 CCTCCTCCCATTCTAGTCCAGATACTCAAAGGAACACGAGTGAATTGTGTGGCATTTTAT 8039
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Db      72756 CCTCCTCCCATTCTAGTCCAGATACTCAAAGGAACACGAGTGAATTGTGTGGCATTTTAT 72815

Qy       8040 CCAAACAACATTTTGTCTTTTTCTGATTAAAAAAAAAAAAAATCTGGCCAGACAGGATGGC 8099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72816 CCAAACAACATTTTGTCTTTTTCTGATTAAAAAAAAAAAAAATCTGGCCAGACAGGATGGC 72875

Qy       8100 TCACGCCTGTAATCCCAGCACTTTAGGAGGCAGAGACGGGTGGATCACCTGAGGTCAGTT 8159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72876 TCACGCCTGTAATCCCAGCACTTTAGGAGGCAGAGACGGGTGGATCACCTGAGGTCAGTT 72935

Qy       8160 CGAGACCAGCTTGGCAAAACCCTGTCTCTACCAAAAATACAAAAATTAGCCCGGCGTGGT 8219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72936 CGAGACCAGCTTGGCAAAACCCTGTCTCTACCAAAAATACAAAAATTAGCCCGGCGTGGT 72995

Qy       8220 GGCAGATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGCGAATCACTTGGACCCG 8279
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72996 GGCAGATGCCTGTAATCCCAGCTACTAGGGAGGCTGAGGCAGGCGAATCACTTGGACCCG 73055

Qy       8280 GGAGGCAGAGGTTGCAGCAAGCTGAGATTGTGCCATTGCACGCCAGCCTGGGCGACAGAG 8339
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73056 GGAGGCAGAGGTTGCAGCAAGCTGAGATTGTGCCATTGCACGCCAGCCTGGGCGACAGAG 73115

Qy       8340 CGAGCCTGGACGACAGAGCGAGACTCCATGTCAAAAAAAATAAAATAAAAACAAAAAATC 8399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73116 CGAGCCTGGACGACAGAGCGAGACTCCATGTCAAAAAAAATAAAATAAAAACAAAAAATC 73175

Qy       8400 CTATTCCCCTTCTGTAGAAAACTTGGATGGGACAGCAAAACATAAAGAAAAAAGCCAGAA 8459
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73176 CTATTCCCCTTCTGTAGAAAACTTGGATGGGACAGCAAAACATAAAGAAAAAAGCCAGAA 73235

Qy       8460 ATCCCCGAAATCCTACTCCTCGGAAATAGCGACGGGGCTCACATTTAGCAGTACATCTCA 8519
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Db      73236 ATCCCCGAAATCCTACTCCTCGGAAATAGCGACGGGGCTCACATTTAGCAGTACATCTCA 73295

Qy       8520 ATCCGTTCTAGGAGAAGGGCACTTGGGGTGTGACATGCCTGGTTTTGAATTCTGGCTCTG 8579
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73296 ATCCGTTCTAGGAGAAGGGCACTTGGGGTGTGACATGCCTGGTTTTGAATTCTGGCTCTG 73355

Qy       8580 CTACTGCCTAACTGTGGGTTCTTGGGTGAGTCACTTTGCCTCCAAAGGCATCAGTTTCCT 8639
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Db      73356 CTACTGCCTAACTGTGGGTTCTTGGGTGAGTCACTTTGCCTCCAAAGGCATCAGTTTCCT 73415

Qy       8640 CATCTGTTAGGTGAGATTATACAGACTGGCCTAGCAGGGAAGCAGTGAGGATGGCATTAA 8699
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73416 CATCTGTTAGGTGAGATTATACAGACTGGCCTAGCAGGGAAGCAGTGAGGATGGCATTAA 73475

Qy       8700 ATCAAGCACTAATCCAGGGTCTGGCATAAAATAGGCATTCAAACATTCCTTTAGGGCTTT 8759
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73476 ATCAAGCACTAATCCAGGGTCTGGCATAAAATAGGCATTCAAACATTCCTTTAGGGCTTT 73535

Qy       8760 ACAGTGCACACCTGAGGTTTAGAGACAGTTCCCCCCCCACACCCTCTTGAGCCTTGTCCTT 8819
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73536 ACAGTGCACACCTGAGGTTTAGAGACAGTTCCCCCCCCACACCCTCTTGAGCCTTGTCCTT 73595

Qy       8820 CCTGGAATTTTTGGCCTTCTTGAGAGCTTCCTTGATTTTCTTATGACAGCCATGAAGCCA 8879
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73596 CCTGGAATTTTTGGCCTTCTTGAGAGCTTCCTTGATTTTCTTATGACAGCCATGAAGCCA 73655

Qy       8880 CAGTGGCTTTTGGGGATCCATTATTTCTCAGAAGGTGCTTGGAGCGGCAGAAGGTTCTAC 8939
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73656 CAGTGGCTTTTGGGGATCCATTATTTCTCAGAAGGTGCTTGGAGCGGCAGAAGGTTCTAC 73715
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Db      75876 GCTGGGGCGGGATTTGGGGCCCTCAGGTCTGCTTCTGCCCTCATAGGCAACCCACCACAT 75935

Qy      11160 AACCCCATCCTAGGATTGCAGGAGATACAGCTCTAGATAAGAATATCCACCAGTCGGTGA 11219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      75936 AACCCCATCCTAGGATTGCAGGAGATACAGCTCTAGATAAGAATATCCACCAGTCGGTGA 75995

Qy      11220 GTGAGCAGATCAAGAAGAACTTTGCCAAGAGCAAGTGGAAGGTGAGTCCATATCCCTAGT 11279
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Db      75996 GTGAGCAGATCAAGAAGAACTTTGCCAAGAGCAAGTGGAAGGTGAGTCCATATCCCTAGT 76055

Qy      11280 TCTGGTCCCAGCCTCCCCAGGACTCCTCCCCATCCCTACCCAGGCTCAGCTTGCACAGCA 11339
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Db      76056 TCTGGTCCCAGCCTCCCCAGGACTCCTCCCCATCCCTACCCAGGCTCAGCTTGCACAGCA 76115

Qy      11340 CCTGGCATCACACTGGGCACACAGTAACTGCTTAGGGATCCTTACTGAAGGACTTCATTC 11399
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Db      76116 CCTGGCATCACACTGGGCACACAGTAACTGCTTAGGGATCCTTACTGAAGGACTTCATTC 76175

Qy      11400 ATTCACTCTTTCATTCAACAAACACTCCCAACACCTTCTCTATTCCAGAGAGGGTCCCTC 11459
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Qy      11460 ACCTCCAAGTCTAGAGGAAGAAGTCTGTAATTCTTCAGGAGGCATCTGATCCAGCCTATG 11519
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Db      76236 ACCTCCAAGTCTAGAGGAAGAAGTCTGTAATTCTTCAGGAGGCATCTGATCCAGCCTATG 76295

Qy      11520 GGGTCCGAGAAAGGTCATAAAAGTGGTGATGACCTGACAGAGCTGTCAGTTAAGTAGGAA 11579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76296 GGGTCCGAGAAAGGTCATAAAAGTGGTGATGACCTGACAGAGCTGTCAGTTAAGTAGGAA 76355

Qy      11580 TTAGTGAGGCATAGCGGAATAATGTCTATAGCCATTCCGGGAAGTGCAAGTGCTAAGCCT 11639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76356 TTAGTGAGGCATAGCGGAATAATGTCTATAGCCATTCCGGGAAGTGCAAGTGCTAAGCCT 76415

Qy      11640 GGCCAGACTGGAGGGGCTGAGGGGACTGAGAGGCAGGAGCCCAATTTAGAGAAGCAGGTA 11699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76416 GGCCAGACTGGAGGGGCTGAGGGGACTGAGAGGCAGGAGCCCAATTTAGAGAAGCAGGTA 76475

Qy      11700 AGGGGCCAGGCCTCTTAGGGCCTCATATGCCACAGAGGAGCACCAACTTGATCCTGAGGG 11759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76476 AGGGGCCAGGCCTCTTAGGGCCTCATATGCCACAGAGGAGCACCAACTTGATCCTGAGGG 76535

Qy      11760 CACTGAGGAGCCCCAGAAGAATCTTAGGCAAGTATTTGCTGCATAGAAAGGGCTCTCAGG 11819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76536 CACTGAGGAGCCCCAGAAGAATCTTAGGCAAGTATTTGCTGCATAGAAAGGGCTCTCAGG 76595

Qy      11820 GCCAGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGTTGGAT 11879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76596 GCCAGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGTTGGAT 76655

Qy      11880 CACCTGAGGTCAGGAGTTCAAGACCATCCTGGCCAACATGGCAAAACCCTGTCTCTACTA 11939
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76656 CACCTGAGGTCAGGAGTTCAAGACCATCCTGGCCAACATGGCAAAACCCTGTCTCTACTA 76715

Qy      11940 AAAATAAAAGAATTAGCCACACATGGTGGTGCGTGCCTGTAATCCCAGCTACTTGGGAAG 11999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76716 AAAATAAAAGAATTAGCCACACATGGTGGTGCGTGCCTGTAATCCCAGCTACTTGGGAAG 76775

Qy      12000 CTGAGGCAGGAGAATTACTTGAACCTCGGAGATGGGGGTTGCAGTGAGCTGAGATCGCGC 12059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76776 CTGAGGCAGGAGAATTACTTGAACCTCGGAGATGGGGGTTGCAGTGAGCTGAGATCGCGC 76835

Qy      12060 CACTGCACTCCAGCCTGGGCAACAAAGTGAGACTCCACCTCAAAAAAAAAAGAAAGAGCT 12119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76836 CACTGCACTCCAGCCTGGGCAACAAAGTGAGACTCCACCTCAAAAAAAAAAGAAAGAGCT 76895

Qy      12120 CTCAGGATGCAGAGAATGGCATGGAGTAAAGACTGGGTGACGCATTAGGAGGCTGTGGCA 12179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76896 CTCAGGATGCAGAGAATGGCATGGAGTAAAGACTGGGTGACGCATTAGGAGGCTGTGGCA 76955

Qy      12180 GAGATACAGGCAGGAGATGGTAAGGGTTTGGAACCACAGTAGCAGCAACAGGGGGCAGAG 12239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76956 GAGATACAGGCAGGAGATGGTAAGGGTTTGGAACCACAGTAGCAGCAACAGGGGGCAGAG 77015
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Qy      12240 AACAGTGGTTGATCCAGGAGTCATTTAGGAGGTGAAACTGACAAGACATGACGATGCAAT 12299
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Db      77016 AACAGTGGTTGATCCAGGAGTCATTTAGGAGGTGAAACTGACAAGACATGACGATGCAAT 77075

Qy      12300 GGATGTTGGGGGAAAGAGATGTCAAGGGCTGGCCCAAGACTGTGGCTGGGAACAGAATGG 12359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77076 GGATGTTGGGGGAAAGAGATGTCAAGGGCTGGCCCAAGACTGTGGCTGGGAACAGAATGG 77135

Qy      12360 ATGGTGGTGGTACCATGACTGAGATGGTTATCACAGGGACAGAAACATGTTTTGGGGGGA 12419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77136 ATGGTGGTGGTACCATGACTGAGATGGTTATCACAGGGACAGAAACATGTTTTGGGGGGA 77195

Qy      12420 TGGTTTTAGTTTTAGACATGGTGAATTTGAGGGGTGTGTGGGACACCTAGGTGGAGATAT 12479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77196 TGGTTTTAGTTTTAGACATGGTGAATTTGAGGGGTGTGTGGGACACCTAGGTGGAGATAT 77255

Qy      12480 TGAATAGAGACACACCTGAGCAAGTTACTTCAGCTTTCTGTGCCTCAGTTTCCTCCTTTG 12539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77256 TGAATAGAGACACACCTGAGCAAGTTACTTCAGCTTTCTGTGCCTCAGTTTCCTCCTTTG 77315

Qy      12540 AAAATGATAATAGTACCTACCTCAAAGACTTTCATGAAGATTAAATGAATTACTACGTAA 12599
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Db      77316 AAAATGATAATAGTACCTACCTCAAAGACTTTCATGAAGATTAAATGAATTACTACGTAA 77375

Qy      12600 AGTGCTTAGAACAGTGCCTGACATACAGTGCTATAGTGTTTGCTATTACATATTAATATG 12659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77376 AGTGCTTAGAACAGTGCCTGACATACAGTGCTATAGTGTTTGCTATTACATATTAATATG 77435

Qy      12660 AATTATAGTTATGTTTCTATTTATATATATAGATACACATACATCTAACATATGTGCGTG 12719
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Db      77436 AATTATAGTTATGTTTCTATTTATATATATAGATACACATACATCTAACATATGTGCGTG 77495

Qy      12720 TGTGTGTGTAAATATATAATAAAGCCTTGTAGAGGTTTTTGGGGGGCTTTAGGGGAATTA 12779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77496 TGTGTGTGTAAATATATAATAAAGCCTTGTAGAGGTTTTTGGGGGGCTTTAGGGGAATTA 77555

Qy      12780 ATAAAATAACTCCTGAATGAAAATAACAGAACAATTGCAAGAATCCCACTGCGCCCCTGC 12839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77556 ATAAAATAACTCCTGAATGAAAATAACAGAACAATTGCAAGAATCCCACTGCGCCCCTGC 77615

Qy      12840 CCCATGACTTGACTCTCTCAAAAGTCCTTTCTCCCCTCTCCCTTCAATGCCTTCAATGCC 12899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77616 CCCATGACTTGACTCTCTCAAAAGTCCTTTCTCCCCTCTCCCTTCAATGCCTTCAATGCC 77675

Qy      12900 AGCAAGCCTTCAATGCCACGGCTGTGGTGCGGCACATGAGGAAACTGCAGCTGGGCACCA 12959
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Db      77676 AGCAAGCCTTCAATGCCACGGCTGTGGTGCGGCACATGAGGAAACTGCAGCTGGGCACCA 77735

Qy      12960 GCCAGGAGGGGCAGGGGCAGACGGCGAGCCATGGGGAGCTGCTGACACCAGTGGCTGGGG 13019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77736 GCCAGGAGGGGCAGGGGCAGACGGCGAGCCATGGGGAGCTGCTGACACCAGTGGCTGGGG 77795

Qy      13020 GTGAGGAGCGGGCTCTGCAGAAGGGCATGGGTGGTCCACAAAGGTGCACCCGGGCTGGAG 13079
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Db      77796 GTGAGGAGCGGGCTCTGCAGAAGGGCATGGGTGGTCCACAAAGGTGCACCCGGGCTGGAG 77855

Qy      13080 TGGAGGGCCTGCCCCTGCGGCCACCTCTGTTCTGTCTTCCCATGCAGGGCCGGCAGCTGG 13139
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Db      77856 TGGAGGGCCTGCCCCTGCGGCCACCTCTGTTCTGTCTTCCCATGCAGGGCCGGCAGCTGG 77915

Qy      13140 CTGTTGCTGTCGAGACTGCTGCGTGGAGCCGGGCACAGAACTGTCCCCCACACTGCCCCA 13199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77916 CTGTTGCTGTCGAGACTGCTGCGTGGAGCCGGGCACAGAACTGTCCCCCACACTGCCCCA 77975

Qy      13200 CCAGCTCTAGGGCCCTGGACCTCGGGTCATGATCCTCTGCGTGGGAGGGCTTGGGGGCAG 13259
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Db      77976 CCAGCTCTAGGGCCCTGGACCTCGGGTCATGATCCTCTGCGTGGGAGGGCTTGGGGGCAG 78035

Qy      13260 CCTGCTCCCCTTCCCTCCCTGAACCGGGAGTTTCTCTGCCCTGTCCCCTCCTCACCTGCT 13319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78036 CCTGCTCCCCTTCCCTCCCTGAACCGGGAGTTTCTCTGCCCTGTCCCCTCCTCACCTGCT 78095
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